

Remarks

Applicant respectfully requests a clarification as to the claim number for which Applicant is required to elect species. While the Examiner has stated that "[c]aim 106 is generic to a plurality of disclosed patentably distinct species of PMPE polypeptides, based on structural and functional differences, comprising" SEQ ID NOs: 17-22, Applicant believes the claim that the Examiner refers to is claim 108 because claim 106 is directed to "[t]he vaccine of claim 103, wherein the additional immunogen is HMW (High Molecular Weight) protein of *Chlamydia trachomatis*."

The undersigned contacted the Examiner by telephone on June 20, 2006 to obtain clarification. The Examiner indicated that she would check the claims to clarify which claim was intended but, despite several phone messages left by the undersigned, the Examiner has not provided clarification. Thus, this reply is made with *the assumption* that claim 108 was intended. If this is incorrect, clarification is respectfully requested.

It is respectfully submitted that this requirement for election of species is unnecessary. Searching all the species of the present invention together does not present a "serious burden" on the Examiner. MPEP § 803 ("If the search and examination of an entire application can be made without serious burden, the examiner **must** examine it on the merits, even though it includes claims to independent or distinct inventions." (emphasis added)).

Searching the species of the present invention together does not create a “serious burden.” The species are all fragments of SEQ ID NO: 2 (*C. trachomatis* pmpE) and thus a search for SEQ ID NO: 2 will reveal any fragments thereof.

In any event, Applicant is entitled to have at least ten sequences searched in the present application. The U.S. Patent and Trademark Office has implemented the following policy with respect to Restriction Requirement practice concerning sequences:

[T]o further aid the biotechnology industry in protecting its intellectual property without creating an undue burden on the Office, the Director has decided *sua sponte* to partially waive the requirements of 37 CFR 1.141 *et seq.* and permit a reasonable number of such nucleotide sequences to be claimed in a single application.

It has been determined that normally ten sequences constitutes a reasonable number for examination purposes. Accordingly, in most cases, **up to ten independent and distinct nucleotide sequences will be examined in a single application without restriction.** MPEP § 803.04 (emphasis added).

Therefore, Applicant is entitled to have at least ten sequences searched in the present application without restriction.

In order to insure compact prosecution should the Examiner agree, Applicant hereby provisionally elects, in addition to SEQ ID NO:5, nine additional sequences, SEQ ID NOs: 6, 7, 8, 9, 10, 11, 12, 21, and 22 to be initially examined. Applicant submits that claims 108 and 118-130 are also readable on SEQ ID NOs: 6, 7, 8, 9, 10, 11, 12, 21, and 22. This election is likewise made without prejudice to or disclaimer of the other claims or inventions disclosed. Upon the identification of otherwise allowable subject matter in a generic or linking claim, Applicant also requests that the Examiner examine any remaining unelected species, according to 37 C.F.R. § 1.141(a). At least for the

reasons noted above, searching these additional sequences together with SEQ ID NO: 5 does not constitute an undue burden.

Applicant reserves all rights in the non-elected species, including the right to file one or more divisional applications covering the subject matter thereof.

It is believed that extensions of time are not required, beyond those that may otherwise be provided for in accompanying documents. However, in the event that additional extensions of time are necessary to prevent abandonment of this application, then such extensions of time are hereby petitioned under 37 C.F.R. § 1.136(a), and any fees required therefor are hereby authorized to be charged to our Deposit Account No. 19-0036.

Respectfully submitted,

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